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 DNSPFV □ LYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFSM  
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 GQIDGLISQLEMDQQAGKLAPANG □ MPTGENVISVAELINAMKQVKHIPESKLTSLAAALDEN  
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S I S L Y Q R F K K T F R Q Y G K V L I P V H L I T S G V W F G T F Y Y A A L K G V N V V P F L E L I G L P D S V V S I L K  
N S Q S G N A L T A Y A L F K I A T P A R Y T V T L G G T S V T V K Y L R S H G Y M S T P P P V K E Y L Q D R M E E T K E L  
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W Q Y E S L K S R V Q S Y F D G I K A D W L D S I R P Q K E G D F R K E I N K W W N N L S D G Q R T V T G I I A A N V L V F  
C L W R V P S L Q R T M I R Y F T S N P A S K V L C S P M L L S T F S H F S L F H M A A N M Y V L W S F S S S I V N I L G Q  
E Q F M A V Y L S A G V I S N F V S Y V G K V A T G R Y G P S L G A S G A I M T V L A A V C T K I P E G R L A I I F L P M F T  
F T A G N A L K A I I A M D T A G M I L G W K F F D H A A H L G G A L F G I W Y V T Y G H E L I W K N R E P L V K I W H E I  
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S M D Q Q I Q N G S S S T S P Y N T D H A Q N S V T A P S P Y A Q P S S T F D A L S P S P A I P S N T D Y P G P H S F D V S  
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E E F A K M K Q E L A E Y L A V F K K T V S S H E V F L Q R L S S H P V L S K D R N F H V F L E Y D Q D L S V R R K N T K  
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>534.1□MANLLKTVVTGCSCPLLSNLGSCCKGLRVKKDFLRTFYTHQELWCKAPVKPGIPIYKQ LTVGVPKEIFQNEKRVALSPAGVQ□NLVKQGFNVVVEGAGEASKFSDDHYRVAGA QIQGAKE VLASDLVVKVRAPMVNPTLGVHEADLLKTS GTLISFIYPAQN□PELLNKLSQRKTTVLTMDQV PRVTIAQGYDALSSMANIAGYKAVVLAANHFRFFTQGITAGKVPPAKILIVGGGVAGL□AS AGAAKSMGAIVRGFDTRA AALEQFKSLGAEPLEVDLKEGEGQGGYAKEMSKEFIEAEMKLFA QQCKEVDILISTALI□PGKKAPVLFNKEMIESMKEG SVVVDLAAEAGGNFETTKPGELYIHKG ITHIGYTDLP SRMATQASXLYSNNITKLLKAI S□PDKDNFYFDVKDDFDFGTMGHVIRGTVM KDGVIFPAPTPKNI PQGAPVKQKTVAELEAEKAATITPFRKTMSTASAYT□AGLTGILGLGI AAPNLAFSQMVTTFGLAGIVGYHTVWGVTPALHSPLMSVTNAISGLTAVGGLALMGGHLYPST TSQGLA□ALAAFISSVNIAGGFLVTQRM LDMFKRPTDPPEYNYLYLLPAGTFVGGYLAALYSG YNIEQIMYLGSLCCV GALAGLST□QGTARLGNALGMIGVAGGLAATLGVLKPGPELLAQMSG AMALGGTIGLTI AKRIQISDLPQLVAAFHSLVGLAAVLT CIA□EYII EYPHFATDAAANLTKI VAYLGTYIGGVTFSGSLIAYGKLQGLLKSAPLLLPGRHLLNAGLLAASVGGIIPFMVDPS□FT TGITCLGAVSALS AVMGVTLTPAIGGADMPVVITVLNSYSGWALCAEGFLLNNNLLTIVGALI GSSGAILS YIMCVAM□NRSLANVILGGYGTSTAGGKPM EISGTHTEINLDNAIDMIREANSI IITPGYGLCAAKAQYPIADLVKMLTEQGKKVRF□GIHPVAGRMPGQLNVLLAEAGVPYDIVLE MDEINHDFPD TDLVLV IGANDTVNSAAQEDPNSI IAGMPVLEVWKS KQVIV□MKRSLGVGYAAVDNPIFYKPNTAMLLG DAKKTC DALQAKVRESYQK□

>535.1□MALLVLGLVSCTFFLAVNGLYSSSDDVIELTPSNFNREVIQSDSLWLVEFYAPWCG HCQRLTP EWKKAATALKDVVKVGA□VDADKHSLGGQYGVQGFP TIKIFGSNKNRPEDYQGGR TGEAIVDAALSALRQLVKDRLGGRSGGYSSGKQGRSDSSSK□DVIELTDDSF DKNVLDSE DV WMVEFYAPWCGHCKNLEPEWAAAASEVKEQTKGKVLA AVDATVNQVLASRYGIRGFPTI□KI FQKGESPV DYGGRTRSDIVSRALDLFSDNAPPELLEI INEDIAKRTCEEHQLCVVAVLPHI LDTGAAGRNSYLEVL□LKLADKYKKKMWGWLWTEAGA QSELETALGIGGFGYPAMAAINARKM K FALLKGSFSEQGINEFLRELSFGRGSTAPVGG□GAFPTIVEREPWDGRDGELPVEDDIDLSD VELDDL GKDEL□

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 I F L V R E S E T T K G A Y S L S I R D W D E I R G D N V K H Y K I R K L D N G G Y I T T R A Q F D T L Q K L V K H Y T E  
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 L K L P Q L V D M A A Q I A D G M A Y I E R M N Y I H R D L R A A N I L V G E N L V C K I A D F G L A R L I E D N E Y T A R  
 Q G A K F P I K W T A P E A A L Y G R F T I K S D V W S F G I L Q T E L V T K G R V P Y P G M V N R E V L E Q V E R G Y R M  
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 GCTCATCGAAAATCCTGCCTTGCTTCGTTGGGCCTATGCAAGAACAATAAATGTCTATC CTA  
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 TCATTTATTATATT ATCAAACTGAGAGGGATAGGAAAGAAAACTTATCCAGGAAGGAAAA  
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>642.1 MRRAALWLWLCALSLQPALPQIVATNLPPEDQDGSGDDSDNFSGSGAGALQDIT  
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 QEATPRPRETTQLPTTHQASTTTATTAQEPATSHPHRDMQPG HHETSTPAGPSQADLHTPHT  
 EDGGPSATERAAEDGASSQLPAAEGSGEQDFTFETSGENTAVVAVEPDRRNQSPVDQGAT GA  
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>643.1 MSLKNEPRVNTSALQKIAADMSNIIENLDTRELHFEGEEVDYDVSPSDPKIQEVYI  
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>647.1□MNL SLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNM  
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>648.1□MSRSPQRALPPGALPRL LQAAPAAQPRALLPQWPRRPGRWPASPLGMKVFRRKAL  
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FGELFNQNPEVFFLYEPVWHVWQKLYPGDAVSLQGAARDMLSALYRCDLSV FQLYSPAGS□GG  
RNLTTLGIFGAATNKVVCSSPLCPAYRKEVVGLVDDRVCCKC P P QRLARFEEECRK YRTLVIK  
GVRVFDVAVLAPLLR□DPALDLKVIHLVRDPRAVASSRIRSRHGLIRESLQVVRSRDPRAHRM  
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QIKQVEEFCYQPM AVLGYERVNSPEEVKDLSKTL LRKPRL□

>649.1□MEKSFATKNEAVQKETLQEGPKQEALQEDPLESFNYVLSKSTKADIGPNLDQLKDD  
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ACDFNL FLEDSADNRQNFSSQSLEHVEKENSLCGSAPNSKAG□FVHSKTCLSWEFSEKDDEPE  
EVVVKAKIRSKARRIVSDGEDEDDSFKDTSSINPFNTSLFQFSSVKQFDASTPKNDISPP□GR  
FFSSQIPSSVNKSMNSRRSLASRRSLINMVL DHVEDMEERLDDSS EAKGPEDYPEEGVEESSG  
EASKYTEEDPSGETL□SSENKSSWLMTSKPSALAQETSLGAPEPLSGEQLVGSPQDKAAEATN  
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[illegible]

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 DSPKAITS LKYM LCKIMLNTPEDVQALVSGKLALRYAGRQTEALKCVAQASKNRSLADFEKA  
 LTDYRAELRDDPIIS THLAKLYDNLLEQNLI RVI EPFSRVQIEHISSLIKLSKADVERKLSQ  
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>653.1 MRS PRTRGRSGRPLSLLLALLCALRAKVCGASGQFELEILSMQNVNGELQNGNCCG  
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 EETPFFLLTGALDARGNNVEKPLELRIKVLNDINDNEPVFTQ □ DVFVGSVEELSAHTLVMKI  
 NATDADEPNTLSKISYRIVSLEPAYPPVFYLNKDTGEIYTTSVTLDREEHSSYTTLTVEA □ RD  
 GNGEVTDKPVKQAQVQIRILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADDEIGSDNW  
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>656.1 □ MATSRYEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGGLPISTVRE  
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>657.1 □ MDSGTRPVGSCCSSPAGLSREYKLVMLGAGGVGKSAMTMQFISHRFPEDHDPTIED  
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 YRVRRTD DTPVVLVGNKSDLKQLRQVTKEEGLALAREFSCPF □ FETSAAYRYI DDVFHALVR  
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ACGTGAAGAAGCTG GAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCATC  
ACCACCAAGAGCGTGTCCAGGTACCGAGGTCA GGAGCACTGCCTGCACCCCAAGCTGCAGAG  
CACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGG TCTACGAAGAAT  
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>720.1 MEFGLSWVFLVALLRGVQCQAQLVESGGGVVQPGSSSLRLSCAASGFRFSNYGMHW  
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VEPKSCDKHTCTPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA  
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSD  
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>721.1□MSSDFPHYNFRMPNIGFQNLPLNIYIVVFGTAIFVFILSLLFCCYLIRLRHQAHKE  
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>722.1□MSLHSTHNRNNSGDILDIPSSQNSSSLNALTHSSRLKLHLKSDMSECENDDPLLRS  
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LTLQORRAKTDSAEEKWKTAEIDSVKMTLNVGGETENNGVSKES□RTNVRIVNNAKNSFVASSVP  
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NRMSNLQVKQRPKSS□FLANKQERSAENTILPEEETVVQNTSAGKDPLKVENŠQVTVAVRVRP  
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GDRLKEGVSINKSLLTLGKVISAL□SEQANQRSVFI PYRESVLTWLLKESLGGNSKTAMIATI  
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>723.1□MELEELGIREECGVFGCIASGEWPTQLDVPHVİTLGLVGLQHRGQESAGİVTSDGS  
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PTAYŠLLİMRDVIYAVRDPYGNRPLCİGRİPVSDİNDKEKKTSETEGWVVSŠESCSFL□Sİ  
GARYYREVLPGEİVEİSRHNVTLDİİSRSEGNPVAFCİFEYVYFARPDŠMFEDQMVYTVRYR  
CGQQLAİEAPVDADL□VŠTVPESATPAALAYAGKCGLPYEVLCNRYVGRTFİQPNMRLRQL  
GİAKKFGVLSDNFKGKRİVLVDDŠİVRGNTİSP□İİKLLKESGAKEVHIRVASPPIKYPCFMG  
İNİPTKEELİANKPEFDHLAİYLGANSVVYLSVEGLVSSVQEGİKFKKQKE□KKHDİMİQENG  
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>724.1□MISSKPRLVVPYGLKTLLEGISRAVLKTNPSNINQFAAAYFQELTMYRGNTTMDIK  
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TTQFPSVYAVPGTEQTEAVGGLSSKPATPKTTTTPPSSPPPTA□VSPEFAYVPADPAQLAAQML  
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VDLGSQPKENEAEPSTASSVPLQDEQEPPAYDQAPEVTLQADIEVMSTVHISSVYNDVPVTEG  
VVYIEQLPEQIVIPF□TDQVACLKENEQSKENEQSPRVSPKSVVEKTTSGMSKKSVEVSVKLAQ  
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AE□

>725.1□MQRPGPRLWLVLQVMGSCAAISSMDMERPGDGKCPPIEIPMCKDIGYNMTRMPNLM  
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PIMEQFNFKWPDSDLCKRLPNKNDPNYLCMEAPNNGSDEPTR□GSGLFPPPLFRPQRPHSAQEH  
PLKDGGPGRGGCDNPGKFHHVEKSASCAPLCTPGVDVYWSREDKRFVWVWLAIWAVLCFF□SS  
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STGCTLVFLVLVYFYG□MASSLWVVLTLTWFLAAGKKWGHEAIEANSSYFHAAWAI PAVKTI  
LILVMRRVAGDELTVGCYVGSMDVNALTGFVLI□PLACYLVIGTSFILSGFVALFHIRRVMKT  
GGENTDKLEKLMVRIGLFSVLYTVPATCVIACYFYERLNMMDYWKILAAQHK□CKMNNQTKTLD  
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>726.1□MSDIGDWFRSIPAITRYWFAATVAVPLVGLGLISPAYLFLWPEAFLYRFQIWRPI  
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QLLMIPLIMSVLYVWAQNLNRMIVSFWFGTRFKACYLPWVIL□GFNYIIGGSVINELIGNLVG  
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GQGFR LGDQ□

>727.1□MATASPRSDTSNNHSGRLQLQVTVSSAKLKRKKNWFGTAIYTEVVVDGEITKTAKS  
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LKLSLENKNGIAQTGELTVVLDGLVIEQENITNCSSSPTIEI□QENGDALHENGEP SARTTAR  
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NGESSFAPT DNASVTGTPV VSEENALSPNCTSTTVEDPPVQEILTSSENNECIPSTSAELES  
EARSILEPDTSNSRS□SSAFEAAKSRQPDGCM DPVRQQSGNANTETLPSGWEQRKDPHGRTYY  
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RYLCQS□NALPSHV KINVS RQTLFEDSFQQIMALKPYDLRRRLYVIFRGEGLDYGGLAREWF  
FLLSHEVLNPMYCLFEYAGKNNYC□LQINPASTINPDHLSYFCFIGRFIAMALFHGKFIDTGF  
SLPFYKRMLSKKLTIKDLESIDTEFYNSLIWIRDNNIEECGL□EMYFSVDMEILGKVTSHDLK  
LGGSNIILVTEENKDEYIGLMTEWRFSRGVQEQTKAFLDGFNEVVPLQWLQYFDEKELEV M□LC  
GMQEVLDLADWQRNTVYRHYTRNSKQIIWFWQFVKETDNEVRMRL LQFVTGTCRLPLGGFAELM  
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>728.1□MDRSKENCISGPVKATAPVGGPKRVLVLTQQFPCQNPLPVNSGQAQRVLCPSNSSQR  
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KMKNQKEA VALED FEIGRPLGKGKFGNVYLAREKQSKFILAL□KVL FKAQLEKAGVEHQ LRRE  
VEIQSHLRHPNILRLYGYFHDATRVYLI EYAPLGTVYRELQKLSKFDEQRTANLYNRIA□NA  
LSYCHSKRVIHRDIKPENLLLSAGELKIADFGWSVHAPSSRRTTLCGTL DYLPPEMIEGRMH  
DEKVDLWSLGVLCYE□FLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNP  
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>729.1□MEDYTKIEKIGEGTYGVVYKGRHKTTGQVVAMKKIRLESEEEGVPSTAIRESILLK  
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CHSRRVLHRDLKPQNLLIDDKGTIKLADFG LARAFGIPIRVY□THEVVTLWYRSPEVLLGSAR  
YSTPVDIWSIGTIFAE LATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKNT□FP  
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>73.1□ATGCTGCCCTGCTTCCAACTGCTGCGCATAGGGGGCGGCAGGGGCGGTGATCTCTAC  
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ATGCCGAGCCCCGGGGTGATGACTGGAGGGTCAGCCTGGAAGACCACAGCAGCCAAGGT□ACT  
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CGGCC□CCAGCCCCCTCACCTTCTCCCCTAGTTGGGGTGGACCAAAGAGCCTGCCTGTTCCCGC  
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CTTATGGAGCCCAGGAAGAACTCCGTGTAGACAAAGCCCCACTGACTCCCACTGGAAA□TGC  
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>730.1□MPKKKPTPIQLNPAPDGS AVNGTSSAETNLEALQKKLEEELELDEQQRKRLEAFLTQ  
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HECN SPYIVGFYGA FYSDGEISICMEHMDGGS LDQVLKKAGR□IPEQILGKVSIAVIKGLTYL  
REKHKIMHRDVKPSN ILVNSRGEIKLCDFGVSGQLIDSMANSFVGTRSYMSPERLQGTHY□SV  
QSDIWSMGLSLVEMAVGRYP I PPPDAKELELMFGCQVEGDAAETPPRP RTPGRPLSSYGMDSR  
PPMAIFELLDYIVNE□PPPKLP SGVFSLEFQDFVNKCLIKNPAERADLKQLMVHAFIKRSDAE  
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>731.1□MSHKQIYYSDKYDDEEF EYRHVMLPKDIAKLVPKTHLMSESEWRNLGVQQSQGWVH  
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>732.1 M L A S S S R I R A A W T R A L L L P L L L A G P V G C L S R Q E L F P F G P G Q G D L E L E D G D D F V S P A  
 L E L S G A L R F Y D R S D I D A V Y V T T N G I I A T S E P P A K E S H P G L F P P T F G A V A P F L A D L D T T D G L G  
 K V Y Y R E D L S P S I T Q R A A E C V H R G F P E I S F Q P S S A V V V T W E S V A P Y Q G P S R D P D Q K G K R N T F Q  
 A V L A S S D S S S Y A I F L Y P E D G L Q F H T T F S K K E N N Q V P A V V A F S Q G S V G F L W K S N G A Y N I F A N D  
 R E S I E N L A K S S N S G Q Q G V W V F E I G S P A T T N G V V P A D V I L G T E D G A E Y D D E D E D Y D L A T T R L G L  
 E D V G T T P F S Y K A L R R G G A D T Y S V P S V L S P R R A A T E R P L G P P T E R T R S F Q L A V E T F H Q Q H P Q V  
 I D V D E V E E T G V V F S Y N T D S R Q T C A N N R H Q C S V H A E C R D Y A T G F C C S C V A G Y T G N G R Q C V A E G  
 S P Q R V N G K V K G R I F V G S S Q V P I V F E N T D L H S Y V V M N H G R S Y T A I S T I P E T V G Y S L L P L A P V G  
 G I I G W M F A V E Q D G F K N G F S I T G G E F T R Q A E V T F V G H P G N L V I K Q R F S G I D E H G H L T I D T E L E G  
 R V P Q I P F G S S V H I E P Y T E L Y H Y S T S V I T S S S T R E Y T V T E P E R D G A S P S R I Y T Y Q W R Q T I T F Q  
 E C V H D D S R P A L P S T Q Q L S V D S V F V L Y N Q E E K I L R Y A F S N S I G P V R E G S P D A L Q N P C Y I G T H G  
 C D T N A A C R P G P R T Q F T C E C S I G F R G D G R T C Y D I D E C S E Q P S V C G S H T I C N N H P G T F R C E C V E  
 G Y Q F S D E G T C V A V D Q R P I N Y C E T G L H N C D I P Q R A Q C I Y T G G S S Y T C S C L P G F S G D G Q A C Q D  
 V D E C Q P S R C H P D A F C Y N T P G S F T C Q C K P G Y Q G D G F R C V P G E V E K T R C Q H E R H I L G A A G A T D P  
 Q R P I P P G L F V P E C D A H G H Y A P T Q C H G S T G Y C W C V D R D G R E V E G T R T R P G M T P P C L S T V A P P I  
 H Q G P A V P T A V I P L P P G T H L L F A Q T G K I E R L P L E G N T M R K T E A K A F L H V P A K V I I G L A F D C V D  
 K M V Y W T D I T E P S I G R A  
 S L H G G E P T T I I R Q D L G S P E G I A V D H L G R N I F W T D S N L D R I E V A K L D G T Q R R V L F E T D L V N P R  
 G I V T D S V R G N L Y W T D W N R D N P K I E T S Y M D G T N R R I L V Q D D L G L P N G L H F D A F S S Q L C W V D A G  
 T N R A E C L N P S Q P S R R K A L E G L Q Y P F A V T S Y G K N L Y F T D W K M N S V V A L D L A I S K E T D A F Q P H K Q  
 T R L Y G I T T A L S Q C P Q G H N Y C S V N N G G C T H L C L A T P G S R T C R C P D N T L G V D C I E R K

>733.1 M P K S K E L V S S G S S G S D S D S E V D K K L K R K K Q V A P E K P V K K Q K T G E T S R A L S S S K Q S S  
 S S R D D N M F Q I G K M R Y V S V R D F K G K V L I D I R E Y W M D P E G E M K P G R K G I S L N P E Q W S Q L K E Q I S  
 D I D D A V R K L

>734.1 M C Y G K C A R C I G H S L V G L A L L C I A A N I L L Y F P N G E T K Y A S E N H L S R F V W F F S G I V G G  
 G L L M L L P A F V F I G L E Q D D C C G C C G H E N C G K R C A M L S S V L A A L I G I A G S G Y C V I V A A L G L A E G  
 P L C L D S L G Q W N Y T F A S T E G Q Y L L D T S T W S E C T E P K H I V E W N V S L F S I L L A L G G I E F I L C L I Q  
 V I N G V L G G I C G F C C S H Q Q Y D C

>735.1 M G K S L S H L P L H S S K E D A Y D G V T S E N M R N G L V N S E V H N E D G R N G D V S Q F P Y V E F T G R  
 D S V T C P T C Q G T G R I P R G Q E N Q L V A L I P Y S D Q R L R P R R T K L Y V M A S V F V C L L L S G L A V F F L F P  
 R S I D V K Y I G V K S A Y V S Y D V Q K R T I Y L N I T N T L N I T N N N Y Y S V E V E N I T A Q V Q F S K T V I G K A R  
 L N N I S I I G P L D M K Q I D Y T V P T V I A E E M S Y M Y D F C T L I S I K V H N I V L M M Q V T V T T T Y F G H S E Q  
 I S Q E R Y Q Y V D C G R N T T Y Q L G Q S E Y L N V L Q P Q Q

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 QKAEPLERLQSQHRQFOARVSRQTLLALEKEEEEEVFESSVPQRSTLAEKSKGKKTARA PI  
 IRVGGALKAPSQNRGLQNPFPQQMQNNSRITVFDENADEASTAELSKPTVQPWIA PPM PRAKE  
 NELQAGPWNTGRSLE HRPGRNTASLIAVPAVLPSFTPYVEETAQQPVMT PCKIEPSINHILS  
 TRKPGKEEGDSLQRVQSHQQASEEKKEKMMYCK EKIYAGVGEFSFEEIRAEVFRKKLKEQRE  
 AELLTSAEKRAEMQKQIEEMEKKLKEIQTTQQERTGDQQEETMPTKETTKL QIASESQKIPG  
 MTLSSSVCQVNCCARETSLAENIWQEQPHSKGPSVPFSIFDEFLLSEKKNKSPADPPRVLAQ  
 RRPLAV LKTSESITSNEDVSPDVCDEFTGIEPLSEDAI ITGFRNVTICPNPEDTCDFAARA  
 FVSTPFHEIMSLKDLPSDPERLLP EEDLDVKTSEDQQTACGTIYSQTLSIKKLSPI IEDSRE  
 ATHSSGFGSGSSASVASTSSIKCLQIPEKLELTNETSENPTQS PWCSQYRRQLLKSLELSAS  
 AELCIEDRPMPKLEIEKEIEELGNEDYCIKREYLICEDYKLFVWVAPRNSAELTVIKVSSQP VP  
 WDFYINLKLKERLNEDFDHFCSCYQYQDGCIVWHQYINCFTLQDLLQHSEYITHEITVLI IYN  
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>737.1 MKLVSVAMLYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGL  
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>738.1 MADGGSERADGRIVKMEVDYSATVDQRLPECAKLAKEGRLQEVIETLLSLEKQTRT  
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 PIKLRLIDTLRMVTEGKIYVEIERARLT KT LATIKEQNGDVKEAASILQELQVETYGSMEKK  
 ERVEFILEQMRLCLAVKDYIRTQII SKKINTKFFQEENTEKLKLKYNNLMIQLDQHEGSY LS  
 ICKHYRAIYDTPCIQAESEKWQALKS VVLYVILAPFDNEQSDLVHRISGDKKLEEIPKYKDL  
 LKLFTTMELMRWSTL VEDYGMELRKGSLESPATDVFGSTE EGEKRWKDLKNRVVEHNIRIMA  
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>739.1 MQRASRLKRELHMLATEPPPGITCWQDKDQMDDLRAQILGGANTPYEKG VFKLEVI  
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 ELDTTLQRADCLVPRNSYVRLRHLCTNTWVTS TSIPIDTDEERPVMKIGTCQTKEDKEAF  
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 MTQMVLRSRGSIFPMSVPDVPSSIHPKQGSPT EHDVTVMDTKLKIIEILQFILSVRLDYRI  
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 IYTSNHIWKL FENFLVDMARVCNTTDRKHADIFLEKCVTESIMNIVSGFFNSPFSN STSLQ  
 THQPVFIQLLQSAFRIY NCTWPNPAQKASVESCI RTLAEVAKNRGIAIPVDLDSQVNTLFMK  
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 GASELVID VIVNTKNDRI FSEGIFLGIALLEGNTQTQYSFYQQLHEQKKSEKFFKVLYDRM  
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 YANHTAQIEIVRHDRTEMQ IVFPVPNICEYLTRESKCRVFNTTERDEQGSKVNDFFQQTEDL  
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 AKENCSP TIPASNTADEEYEDGIERTCD TLLMCIVTVLNQGLRNGGGVGDVLRPSKDEPLF  
 AARVVYDLLFYFIVIIIVLNLI FGVII DT FADLRSEKQKKEEILKT TCFICGLERDKFDNKT  
 VSFEH IKSEHNMWHYLYFIVLVKV KDPTEYTG PESYVAQMIVEKNLDWFPRMRAMSLVSNEG  
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 □

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 FAQAYARGISRTKYWELIYEDSVDLIAKLPCVAAKIYRNLYWEGSGIGAIDSNDWSHNF TN  
 MLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALS DPYLSFAAAMNGLAGPLHGLAN  
 QEVLVWLTQLQKEVG KDVSDEKLRDIWNLTNSGRVVPGYGHAVLRKTDPRYTCQREFALKH  
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>853.1 MALLTAAARLLGTKNASCLVLAARHASASSTNLKDILADLIPKEQARIKTFRQQHG  
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 FAQAYARGISRTKYWELIYEDSVDLIAKLPCVAAKIYRNLYWEGSGIGAIDSNDWSHNF TN  
 MLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLAN  
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>854.1 MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAF  
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>855.1 MGGLWRPGWRCVPFCGWRWIHPGSPTRAAERVEPFLRPEWSGTGGAERGLRWLGTW  
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 LYCQTTGLGGSAVAGHASDKIENMPVKDRIIKISFNADVHA SLQWNFRPQQTEIYVVPGET  
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 IRWRPASPPVVKLEV FYNSEYSMPSTHAMSGETAIPISMVLLTYGRWQYPLIYGLILIPC WC  
 SLVCLSRIYMGMH SILDIIAGFLYTIILAVFYPFVDLIDNFNQTHKYAPFIIIGLHLALGIF  
 SFTLDTWSTSRGDTA EILGSGAGIACGSHVTYNMGLVLDPSLDTLPLAGPPITVTLFGKAIL  
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>857.1 MALQIPGGFWAAAVTVMLVMLSTPVAEARDFPKDFLVQFKGMCYFTNGTERVRGVA  
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 QAYTQFGGKRPFVGSLLYIGWDKHYGFQLYQSDPSGNYGGWK ATCIGNNSAAAVSMLKQDYK  
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>859.1□MKGDT RHLNGEEDAGG REDSILVNGACSDQSSDSPPILEAIRTP EIRGRRSSRLS  
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PSPRSTRGRQGRNHVDESPVEFPAT RSLRRRATASAGTPWPS□PPSSYLTIDLTD DTDTHGT  
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RKLES RKYENKTRRRTADDSATSDYCPAPKRLK□TNCYNNGKDRGDEDQ SREQMASDVANNKS  
SLEDGCLSCGRKNPVSFHPLFEGGLCQTCRDRFLELFYMYDDDGYQSYCTV□CCEGRELL LCS  
NTSCC RCFCVECLEVLVGTGTAAEAKLQEPWSCYMCLPQRCHGVLR RRKDOWNVRLQAFFTSDT  
GLEYE A□PKLYPAIPAARRRPIRVLSLFDGIATGYLV LKELGIKVGKYVASEVCEESI AVGTV  
KHEGNIKYVNDVRNITKKNIEEWG□PFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHL  
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GMNRPV IASKNDKLELQDCLEYNRIAKLKKVQTITTKSNSIKQGKNQLFPVVMNGKEDVL□WC  
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>86.1 □TAAAGTAACAACGGTAATAAAGAGTTTTCACTCTCCAAATCACAGGGCTCCTAGGTA  
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TCCCTCAGGACGGAAGCCACTGGCTTAGTATGAAGGATATAGTTGAGGTTCTCAGTGAC □CGG  
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CTGAACCTCTTTAAGGAGAGCAAGTTTGATGCTCTTTTTCACAGACCCAGCCTTACCCTGTGGG  
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CAATGGTCTCAGAAATTCCAGAGAAGAAAGCTAT □GGCAATTGCTGATGCTTTGGGCAAAAAC  
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CCATGCT □GGTTCCCATGGTGTATTATGAAAGCATATGCAATGGCGTTCCCATGGTGATGATGC  
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>860.1 □MLRLYLVLVMGVSAFTLQPAHTGAARSCRFRGRHYKREFRLEGE PVALRCPQVPYW  
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MSIELRVFENTDAFLPFISYPQILTLSTSGVLVCPDLSEFTR □DKTDVKIQWYKDSL LLDKDN  
EKFLSVRGTT HLLVHDVALEDAGYYRCVLTFAHEGQQYNITRSIELRIKKKKEETIPVII □SP  
LKTISASLGSRLTIPCKVFLGTGTPLT TMLWWTANDTHIESAYPGGRVTEGPRQEYSENNENY  
IEVPLIFDPVTREDL □HMDFKCVVHNTLSFQTLRTTVKEASSTFSWGIVLAPLSLAFLVLGGI  
WMHRRCKHRTGKADGLTVLWPHHQDFQSYPK □

>861.1 M K L A A M I K K M C P S D S E L S I P A K N C Y R M V I L G S S K V G K T A I V S R F L T G R F E D A Y T P T  
 I E D F H R K F Y S I R G E V Y Q L D I L D T S G N H P F P A M R R L S I L T G D V F I L V F S L D N R D S F E E V Q R L R  
 Q Q I L D T K S C L K N K T K E N V D V P L V I C G N K G D R D F Y R E V D Q R E I E Q L V G D D P Q R C A Y F E I S A K K  
 N S S L D Q M F R A L F A M A K L P S E M S P D L H R K V S V Q Y C D V L H K K A L R N K K L L R A G S G G G G G D P G D A  
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>862.1 M D C G S V G G Q R T Q R L P G R Q R L L F L P V G L S G R P G G S E T S A R R C P S A L S D G L G A L R P R A  
 P A A R G G V S R A S P L L L L L V P S P R L A A A A P R R Q L G D W E R S R L G Y A A P P A G R S G A W R C S P G V A A  
 A A G A L P Q Y H G P A P A L V S C R R E L S L S A G S L Q L E R K R R D F T S S G S R K L Y F D T H A L V C L L E D N E S  
 H S F I Q A G V Q W H S L G L L Q P P P G F K R S S H L I L L S S W D Y R H A P P H L D N F S V F L L E T G F H H V G Q A  
 G L K L L T S S D P P T L A S

>863.1 M E A G E G K E R V P K Q R Q V L I F F V L L G I A Q A S C Q P R H Y S V A E E T E S G S F V A N L L K D L G L  
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 F Q A E L R I R D V N D H S P V F L D K E I L L K I P E S I T P G T T F L I E R A Q D L D V G T N S L Q N Y T I S P N F H F  
 H L N L Q D S L D G I I L P Q L V L N R A L D R E E Q P E I R L T L T A L D G G S P P R S G T A L V R I E V D I N D N V P  
 E F A K L L Y E V Q I P E D S P V G S Q V A I V S A R D L D I G T N G E I S Y A F S Q A S E D I R K T F R L S A K S G E L L L  
 R Q K L D F E S I Q T Y T V N I Q A T D G G G L S G T C V V F V Q V M D L N D N P P E L T M S T L I N Q I P E N L Q D T L I  
 A V F S V S D P D S G D N G R M V C S I Q D D L P F F L K P S V E N F Y T L V I S T A L D R E T R S E Y N I T I T V T D F G  
 T P R L K T E H N I T V L V S D V N D N A P A F T Q T S Y T L F V R E N N S P A L H I G S V S A T D R D S G T N A Q V T Y S  
 L L P P Q D P H L P L A S L V S I N A D N G H L F A L Q S L D Y E A L Q A F E F R V G A A D R G S P A L S S E A L V R V L V L  
 D A N D N S P F V L Y P L Q N G S A P C T E L V P R A A E P G Y L V T K V V A V D G D S G Q N A W L S Y Q L L K A T E P G L  
 F G V W A H N G E V R T A R L L R E R D A A K Q R L V V L V K D N G E P P R S A T A T L H V L L V D G F S Q P Y L L L P E A  
 A P A Q A Q A D L L T V Y L V V A L A S V S S L F L F S V L L F V A V R L C R R S R A A S V G R C S V P E G P F P G Q M V D  
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>864.1 M V N E G P N Q E E S D D T P A P E S A L Q A D P S V S V H P S V S V H P S V S I N P S V S V H P S S S A H P S  
 A L A Q P S G L A H P S S S G P E D L S V I K V S R R R W A V V L V F S C Y S M C N S F Q W I Q Y G S I N N I F M H F Y G V  
 S A F A I D W L S M C Y M L T Y I P L L P V A W L L E K F G L R T I A L T G S A L N C L G A W V K L G S L K P H L F P V T  
 V V G Q L I C S V A Q V F I L G M P S R I A S V W F G A N E V S T A C S V A V F G N Q L G I A I G F L V P P V L V P N I E D  
 R D E L A Y H I S I M F Y I I G G V A T L L L I L V I I V F K E K P K Y P P S R A Q S L S Y A L T S P D A S Y L G S I A R L F  
 K N L N F V L L V I T Y G L N A G A F Y A L S T L L N R M V I W H Y P G E E V N A G R I G L T I V I A G M L G A V I S G I W  
 L D R S K T Y K E T T L V V Y I M T L V G M V V Y T F T L N L G H L W V V F I T A G T M G F F M T G Y L P L G F E F A V E L  
 T Y P E S E G I S F G L L N I S A Q V F G I I F T I S Q G Q I I D N Y G T K P G N I F L C V F L T L G A A L T A F I K A D L  
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>865.1 M E L S E P I V E N G E T E M S P E E S W E H K E E I S E A E P G G G S L G D G R P P E E S A H E M M E E E E  
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 E T W Y L S W A L D T N Q E E R D K G K T V E V G R A Y F E T E K K H F T I L D A P G H K S F V P N M I G G A S Q A D L A V  
 L V I S A R K G E F E T G F E K G G Q T R E H A M L A K T A G V K H L I V L I N K M D D P T V N W S N E R Y E E C K E K L V  
 P F L K K V G F N P K K D I H F M P C S G L T G A N L K E Q S D F C P W Y I G L P F I P Y L D N L P N F N R S V D G P I R L P  
 I V D K Y K D M G T V V L G K L E S G S I C K G Q Q L V M M P N K H N V E V L G I L S D D V E T D T V A P G E N L K I R L K  
 G I E E E E I L P G F I L C D P N N L C H S G R T F D A Q I V I I E H K S I I C P G Y N A V L H I H T C I E E V E I T A L I  
 C L V D K K S G E K S K T R P R F V K Q D Q V C I A R L R T A G T I C L E T F K D F P Q M G R F T L R D E G K T I A I G K V  
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>866.1 M R A P L L P P A P V V L S L L I L G S G H Y A A G L D L N D T Y S G K R E P F S G D H S A D G F E V T S R S E  
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 N T S D K P K R K K K G G K N G K N R R R N R K K K N P C N A E F Q N F C I H G E C K Y I E H L E A V T C K C Q Q E Y F G E R  
 C G E K S M K T H S M I D S S L S K I A L A A I A A F M S A V I L T A V A V I T V Q L R R Q Y V R K Y E G E A E E R K K L R  
 Q E N G N V H A I A

>867.1 M L P G L A A A A H R C S W S S L C R L R L R C R A A A C N P S D R Q E W Q N L V T F G S F S N V V P C S H P  
 Y I G T L S Q V K L Y S T N V Q E G Q G S Q T L R V E K V P S F E T A E G I G A E L K A P L K Q E P L Q V R V K A V L K K  
 R E Y G S K Y T Q N N F I T G V R A I N E F C L K S S D L E Q L R K I R R R S P H E D T E S F T V Y L R S D V E A K S L E V  
 W G S P E A L A R E K K L R K E A E I E Y R E R L F R N Q K I L R E Y R D F L G N T K P R S R T A S V F F K G P G K V V M V  
 A I C I N G L N C F F K F L A W I Y T G S A S M F S E A I H S L S D T C N Q G L L A L G I S K S V Q T P D P S H P Y G F S N M  
 R Y I S S L I S G V G I F M M G A G L S W Y H G V M G L L H P Q P I E S L L W A Y C I L A G S L V S E G A T L L V A V N E L  
 R R N A R A K G M S F Y K Y V M E S R D P S T N V I L L E D T A A V L G V I I A A T C M G L T S I T G N P L Y D S L G S L G  
 V G T L L G M V S A F L I Y T N T E A L L G R S I Q P E Q V Q R L T E L L E N D P S V R A I H D V K A T D L G L G K V R F K  
 A E V D F D G R V V T R S Y L E K Q D F D Q M L Q E I Q E V K T P E E L E T F M L K H G E N I I D T L G A E V D R L E K E L K  
 K R N P E V R H V D L E I L

>868.1 M A S S N T V L M R L V A S A Y S I A Q K A G M I V R R V I A E G D L G I V E K T C A T D L Q T K A D R L A Q M  
 S I C S S L A R K F P K L T I I G E E D L P S E E V D Q E L I E D S Q W E E I L K Q P C P S Q Y S A I K E E D L V V W V D P  
 L D G T K E Y T E G L L D N V T V L I G I A Y E G K A I A G V I N Q P Y Y N Y E A G P D A V L G R T I W G V L G L G A F G F  
 Q L K E V P A G K H I I T T T R S H S N K L V T D C V A A M N P D A V L R V G G A G N K I I Q L I E G K A S A Y V F A S P G  
 C K K W D T C A P E V I L H A V G G K L T D I H G N V L Q Y H K D V K H M N S A G V L A T L R N Y D Y Y A S R V P E S I K N A  
 L V P

>869.1 M S G I K K Q K T E N Q Q K S T N V V Y Q A H H V S R N K R G Q V V G T R G G F R G C T V W L T G L S G A G K T  
 T I S F A L E E Y L V S H A I P C Y S L D G D N V R H G L N R N L G F S P G D R E E N I R R I A E V A K L F A D A G L V C I  
 T S F I S P F A K D R E N A R K I H E S A G L P F F E I F V D A P L N I C E S R D V K G L Y K R A R A G E I K G F T G I D S  
 D Y E K P E T P E R V L K T N L S T V S D C V H Q V V E L L Q E Q N I V P Y T I I K D I H E L F V P E N K L D H V R A E A E  
 T L P S L S I T K L D L Q W V Q V L S E G W A T P L K G F M R E K E Y L Q V M H F D T L L D D G V I N M S I P I V L P V S A E  
 D K T R L E G C S K F V L A H G G R R V A I L R D A E F Y E H R K E E R C S R V W G T T C T K H P H I K M V M E S G D W L V  
 G G D L Q V L E K I R W N D G L D Q Y R L T P L E L K Q K C K E M N A D A V F A F Q L R N P V H N G H A L L M Q D T C R R L  
 L E R G Y K H P V L L L H P L G G W T K D D D V P L D W R M K Q H A A V L E E G V L D P K S T I V A I F P S P M L Y A G P T  
 E V Q W H C R S R M I A G A N F Y I V G R D P A G M P H P E T K K D L Y E P T H G G K V L S M A P G L T S V E I I P F R V A A  
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>87.1 □GTGCAAGCGATTAAAGTTGGGTAACGCAGGGTTTCCCAGTCACGACGTGTAAACGCGG  
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 CGGTGTGAGGAGCTGTGAAATTAGTTGTAAGTGAATAAGTGTCTGACGGTCTGGATAATGA □AGA  
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 CATTGATAGAAGCAGT  
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 TGTCAATAAACCTGGCTCTTTGGTTAAGGAAAA□

>870.1□MFLLSNKRKTHFGAGIPIMSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGI  
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 ERFDHHC PWGNCV GKRNYRYFYLFILSLSLTIYVFAFNIVYVALKSLKIGFLET  
 LKET□PG  
 TVLEVLI CFFTLWSV VGLTG FHTFLVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL  
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>871.1□MAVWLAQWLGLPLLLVSLWGLLAPASLLRRLGEHIQQFQESSAQGLGLSLGPGAAAL  
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 LSVRQLCGLLLGGGG□NRSHSTPYCGLRRAVQIVLHSLGQKCLSFSRAETVAQLRSTEPQLSG  
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>872.1□MRAPGALLARMSRLLLLLLLKVSASSALGVAPASRNETCLGESCAPTVIQRRGRDA  
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 MYEMIENCSSTAKLAVI WVGA LLLALPEVVL□RQLSKEDLGFSGRAPAERCI IKISPDLPD  
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>873.1□MAARGVIAPVGESLRYAEYLQPSAKRPDADVDQQLVRSLIAVGLGVAALAFAGRY  
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>874.1 M Y S G N R S G G H G Y W D G G G A A G A E G P A P A G T L S P A P L F S P G T Y E R L A L L L G S I G L L G V  
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 F S G S L F G I V S I A T L T V L A Y E R Y I R V V H A R V I N F S W A W R A I T Y I W L Y S L A W A G A P L L G W N R Y I  
 L D V H G L G C T V D W K S K D A N D S S F V L F L F L G C L V V P L G V I A H C Y G H I L Y S I R M L R C V E D L Q T I Q  
 V I K I L K Y E K K L A K M C F L M I F T F L V C W M P Y I V I C F L V V N G H G H L V T P T I S I V S Y L F A K S N T V Y N  
 P V I Y V F M I R K F R R S L L Q L L C L R L L R C Q R P A K D L P A A G S E M Q I R P I V M S Q K D G D R P K K K V T F N  
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>875.1 M R K T R L W G L L W M L F V S E L R A A T K L T E E K Y E L K E G Q T L D V K C D Y T L E K F A S S Q K A W Q  
 I I R D G E M P K T L A C T E R P S K N S H P V Q V G R I I L E D Y H D H G L L R V R M V N L Q V E D S G L Y Q C V I Y Q P  
 P K E P H M L F D R I R L V V T K G F S G T P G S N E N S T Q N V Y K I P P T T T K A L C P L Y T S P R T V T Q A P P K S T  
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>876.1 M A Q R K N A K S S G N S S S S G S G S G S T S A G S S S P G A R R E T K H G G H K N G R K G G L S G T S F F T  
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 V P P E A E P H T E P E E Q V P V E A E P Q N I E D E A K E Q I Q S L L H E M V H A E H V E G E D L Q Q E D G P T G E P Q  
 Q E D D E F L M A T D V D D R F E T L E P E V S H E E T E H S Y H V E E T V S Q D C N Q D M E E M M S E Q E N P D S S E P V  
 V E D E R L H H D T D D V T Y Q V Y E E Q A V Y E P L E N E G I E I T E V T A P P E D N P V E D S Q V I V E E V S I F P V E E  
 Q Q E V P P D T

>877.1 M G Q N D L M G T A E D F A D Q F L R V T K Q Y L P H V A R L C L I S T F L E D G I R M W F Q W S E Q R D Y I D  
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 R N L A L G G G L L L L L A E S R S E G K S M F A G V P T M R E S S P K Q Y M Q L G G R V L L V L M F M T L L H F D A S F F  
 S I V Q N I V G T A L M I L V A I G F K T K L A A L T L V V W L F A I N V Y F N A F W T I P V Y K P M H D F L K Y D F F Q T  
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>878.1 M K K K L V V L G L L A V V L V L V I V G L C L W L P S A S K E P D N H V Y T R A A V A A D A K Q C S K I G R D  
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 F N S S E Q S Q K G G L S V A V P G E I R G Y E L A H Q R H G R L P W A R L F Q P S I Q L A R Q G F P V G K G L A A A L E N  
 K R T V I E Q Q P V L C E V F C R D R K V L R E G E R L T L P Q L A D T Y E T L A I E G A Q A F Y N G S L T A Q I V K D I Q  
 A A G G I V T A E D L N N Y R A E L I E H P L N I S L G D A V L Y M P S A P L S G P V L A L I L N I L K G Y N F S R E S V E S  
 P E Q K G L T Y H R I V E A F R F A Y A K R T L L G D P K F V D V T E V V R N M T S E F F A A Q L R A Q I S D D T T H P I S  
 Y Y K P E F Y T P D D G G T A H L S V V A E D G S A V S A T S T I N L Y F G S K V R S P V S G I L F N N E M D D F S S P S I  
 T N E F G V P P S P A N F I Q P G K Q P L S S M C P T I M V G Q D G Q V R M V V G A A G G T Q I T T A T A L A I I Y N L W F  
 G Y D V K R A V E E P R L H N Q L L P N V T T V E R N I D Q A V T A A L E T R H H H T Q I A S T F I A V V Q A I V R T A G G W  
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>879.1 M A V T V D K P W F Y D M K K V W E G Y P I Q S T I P S Q Y W Y Y M I E L S F Y W S L L F S I A S D V K R K D F  
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 A I V F I I T R L V I L P F W I L H C T L V Y P L E L Y P A F F G Y Y F F N S M M G V L Q L L H I F W A Y L I L R M A H K F  
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>88.1 GCAGCGAGAGCTGGAGGTGTTGGGTCGGGAGACCAGCCATTCGATCCCGCCGCAGGT  
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>977.1 M A L A R A W K Q M S W F Y Y Q Y L L V T A L Y M L E P W E R T V F N S M L V S I V G M A L Y T G Y V F M P Q H  
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>99.1 □TCGGCACGAGCCAAGATGTCTGACATGGAGGATGATTTTCATGTGCGATGATGAGGAG  
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### Patentansprüche

1. Nukleinsäure, insbesondere isolierte Nukleinsäure, enthaltend oder bestehend aus einer Nukleinsäuresequenz gemäß einer der Sequenzen Seq.-ID 1 bis 489.
2. Peptid oder Protein, insbesondere isoliertes Peptid oder Protein, enthaltend eine Aminosäuresequenz codiert durch eine der Nukleinsäuresequenzen Seq.-ID 1 bis 489 oder bestehend hieraus oder enthaltend eine Aminosäuresequenz gemäß einer der Sequenzen Seq.-ID 490 bis 978 oder bestehend hieraus.
3. Verwendung einer Nukleinsäure und/oder eines Peptids oder Proteins nach Anspruch 1 oder 2, zur Detektion von Bronchialkrebs oder zur Detektion eines Risikos der Erkrankung an Bronchialkrebs, wobei eine Bronchial-Gewebeprobe auf differenzielle Transkription der Nukleinsäure oder auf differenzielle Expression des Proteins untersucht wird und/oder wobei die Nukleinsäure und/oder das Peptid oder Protein in Blutserum oder Sputum detektiert wird.
4. Verwendung nach Anspruch 3, wobei eine an die Nukleinsäure oder eine an das Protein oder Peptid bindende Detektorsubstanz, vorzugsweise enthaltend eine Reportergruppe, verwendet wird, wobei Bindung besagter Nukleinsäure und/oder besagten Proteins oder Peptids an die Detektorsubstanz halbquantitativ oder quantitativ detektiert wird.
5. Verwendung einer Nukleinsäure oder eines Proteins oder Peptids nach Anspruch 1 oder 2, zum Screenen nach daran bindenden Substanzen, insbesondere prospektiven Wirkstoffen zur Inhibierung von besagter



Nukleinsäure oder besagtem Protein oder Peptid, oder prospektiven Detektorsubstanzen, wobei eine prospektive Substanz oder eine Mischung solcher prospektiver Substanzen mit besagter Nukleinsäure oder besagtem Protein oder Peptid kontaktiert wird, wobei mit einem Bindungsassay Bindungsereignisse festgestellt werden, und wobei eine bindende prospektive Substanz, ggf. nach Dekonvolution, selektiert wird.

6. Verwendung einer Nukleinsäure oder ein Peptid bzw. Protein nach Anspruch 1 oder 2 inhibierenden oder daran bindenden Substanz, insbesondere identifiziert nach Anspruch 5, zur Herstellung einer pharmazeutischen Zusammensetzung zur Diagnose und/oder Behandlung von Bronchialkrebs.

7. Verwendung nach Anspruch 6, wobei die Substanz ausgewählt ist aus der Gruppe bestehend aus:

- a) Antisense-Oligonukleotide, siRNA, und Ribozyme gegen eine Nukleinsäure nach Anspruch 1,
- b) an ein Peptid oder Protein nach Anspruch 2 bindendes, insbesondere nach Anspruch 5 identifiziertes, organisches Molekül mit einem Molekulargewicht unterhalb 5000, vorzugsweise unterhalb 1000, höchstvorzugsweise unterhalb 300,
- c) Aptamer gegen ein Protein oder Peptid nach Anspruch 2, insbesondere identifiziert nach Anspruch 5,
- d) (monoklonaler) Antikörper, insbesondere humaner oder humanisierter Antikörper, gegen ein Protein oder Peptid nach Anspruch 2,
- e) anti-idiotypische nicht-humane (monoklonale) Antikörper, generiert mittels eines Antikörpers der Untergruppe d), und
- f) vorstehende Substanzen derivatisiert mit einer Reportergruppe, einem Zelltoxin einer immunstimulierenden Komponente und/oder einem Radioisotop.

8. Verwendung nach einem der Ansprüche 6 oder 7, wobei die pharmazeutische Zusammensetzung zur lokalen Applikation in Tumorzellen enthaltendem Gewebe hergerichtet ist.

9. Verfahren zur Diagnose einer Bronchialkrebserkrankung, wobei eine pharmazeutische Zusammensetzung nach einem der Ansprüche 6 bis 8 in der Ausführungsform mit einer Reportergruppe in zu untersuchendes Gewebe in vivo oder in vitro appliziert wird, wobei das zu untersuchende Gewebe dann einer Detektionsverfahrenstufe unterworfen wird, welche sensitiv für die Reportergruppe ist, und wobei im Fall der Detektion eines definierten Mindestwertes (Überexpression in Tumorgewebe) oder eines definierten Maximalwertes (Unterexpression in Tumorgewebe) der Reportergruppe im Gewebe optional das Gewebe als Tumorzellen enthaltend qualifiziert wird, oder wobei eine pharmazeutische Zusammensetzung nach einem der Ansprüche 6 bis 8 in der Ausführungsform mit einer Reportergruppe mit einer Blutserumprobe und/oder einer Sputumprobe kontaktiert wird, wobei die Probe dann einer Detektionsverfahrenstufe unterworfen wird, welche sensitiv für die Reportergruppe ist, und wobei im Fall der Detektion eines definierten Mindestwertes oder eines definierten Maximalwertes der Reportergruppe in der Probe optional Bronchialgewebe des zugeordneten Patienten als Tumorzellen enthaltend qualifiziert wird.

10. Verfahren zur Behandlung einer Bronchialtumor-Erkrankung, wobei eine pharmazeutische Zusammensetzung nach einem der Ansprüche 6 bis 8 in einer physiologisch wirksamen Dosis einem Patienten dargebracht wird.

Es folgt kein Blatt Zeichnungen